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7148.003 Sequence Listing.ST25  
SEQUENCE LISTING

<110> Cummings, Richard D.  
Ju, Tongzhong

<120> CORE1 BETA-3 GALACTOSYLTRANSFERASE SPECIFIC MOLECULAR  
CHAPARONES, NUCLEIC ACIDS, AND METHODS OF USE THEREOF

<130> 7148.003

<150> 60/411,310

<151> 2002-09-13

<160> 16

<170> PatentIn version 3.1

<210> 1

<211> 318

<212> PRT

<213> Homo sapiens

<400> 1

Met Leu Ser Glu Ser Ser Ser Phe Leu Lys Gly Val Met Leu Gly Ser  
1 5 10 15

Ile Phe Cys Ala Leu Ile Thr Met Leu Gly His Ile Arg Ile Gly His  
20 25 30

Gly Asn Arg Met His His His Glu His His His Leu Gln Ala Pro Asn  
35 40 45

Lys Glu Asp Ile Leu Lys Ile Ser Glu Asp Glu Arg Met Glu Leu Ser  
50 55 60

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Lys	Ser	Phe	Arg	Val	Tyr	Cys	Ile	Ile	Leu	Val	Lys	Pro	Lys	Asp	Val	65	70	75	80
Ser	Leu	Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp	Thr	Lys	His	Cys	Asp	Lys	85	90	95	
Ala	Glu	Phe	Phe	Ser	Ser	Glu	Asn	Val	Lys	Val	Phe	Glu	Ser	Ile	Asn	100	105	110	
Met	Asp	Thr	Asn	Asp	Met	Trp	Leu	Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	115	120	125	
Ala	Phe	Asp	Lys	Tyr	Arg	Asp	Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	130	135	140	
Pro	Thr	Thr	Phe	Ala	Ile	Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Lys	145	150	155	160
Lys	Asp	Pro	Ser	Gln	Pro	Phe	Tyr	Leu	Gly	His	Thr	Ile	Lys	Ser	Gly	165	170	175	
Asp	Leu	Glu	Tyr	Val	Gly	Met	Glu	Gly	Gly	Ile	Val	Leu	Ser	Val	Glu	180	185	190	
Ser	Met	Lys	Arg	Leu	Asn	Ser	Leu	Leu	Asn	Ile	Pro	Glu	Lys	Cys	Pro	195	200	205	
Glu	Gln	Gly	Gly	Met	Ile	Trp	Lys	Ile	Ser	Glu	Asp	Lys	Gln	Leu	Ala	210	215	220	
Val	Cys	Leu	Lys	Tyr	Ala	Gly	Val	Phe	Ala	Glu	Asn	Ala	Glu	Asp	Ala	225	230	235	240
Asp	Gly	Lys	Asp	Val	Phe	Asn	Thr	Lys	Ser	Val	Gly	Leu	Ser	Ile	Lys	245	250	255	
Glu	Ala	Met	Thr	Tyr	His	Pro	Asn	Gln	Val	Val	Glu	Gly	Cys	Cys	Ser	260	265	270	
Asp	Met	Ala	Val	Thr	Phe	Asn	Gly	Leu	Thr	Pro	Asn	Gln	Met	His	Val	275	280	285	
Met	Met	Tyr	Gly	Val	Tyr	Arg	Leu	Arg	Ala	Phe	Gly	His	Ile	Phe	Asn				

290

295

300

Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser Asp Asn Asp  
 305 310 315

&lt;210&gt; 2

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga ggatgagcgc      180
atggagctca gtaagagctt tcgagtatac tgtattatcc ttgtaaaacc caaagatgtg      240
agtctttggg ctgcagtaaa ggagacttgg accaaacact gtgacaaagc agagttcttc      300
agttctgaaa atgttaaagt gtttgagtca attaatatgg acacaaatga catgtgggta      360
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ttccttgcac gcccactac gtttgctatc attgaaaacc taaagtattt tttgttaaaa      480
aaggatccat cacagccttt ctatctaggc cacactataa aatctggaga ccttgaatat      540
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ctcaatatcc cagaaaagtg tcctgaacag ggagggatga tttggaagat atctgaagat      660
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gatggaaaag atgtatttaa taccaaactt gttgggcttt ctattaaaga ggcaatgact      780
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ctgactccaa atcagatgca tgtgatgatg tatgggggat accgccttag ggcatttggg      900
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&lt;210&gt; 3

&lt;211&gt; 316

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

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Met Leu Ser Glu Ser Ser Ser Phe Leu Lys Gly Val Met Leu Gly Ser  
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Ile Phe Cys Ala Leu Ile Thr Met Leu Gly His Ile Arg Ile Gly Asn  
20 25 30

Arg Met His His His Glu His His His Leu Gln Ala Pro Asn Lys Asp  
35 40 45

Asp Ile Ser Lys Ile Ser Glu Ala Glu Arg Met Glu Leu Ser Lys Ser  
50 55 60

Phe Arg Val Tyr Cys Ile Val Leu Val Lys Pro Lys Asp Val Ser Leu  
65 70 75 80

Trp Ala Ala Val Lys Glu Thr Trp Thr Lys His Cys Asp Lys Ala Glu  
85 90 95

Phe Phe Ser Ser Glu Asn Val Lys Val Phe Glu Ser Ile Asn Met Asp  
100 105 110

Thr Asn Asp Met Trp Leu Met Met Arg Lys Ala Tyr Lys Tyr Ala Tyr  
115 120 125

Asp Gln Tyr Arg Asp Gln Tyr Asn Trp Phe Phe Leu Ala Arg Pro Thr  
130 135 140

Thr Phe Ala Val Ile Glu Asn Leu Lys Tyr Phe Leu Leu Lys Lys Asp  
145 150 155 160

Gln Ser Gln Pro Phe Tyr Leu Gly His Thr Val Lys Ser Gly Asp Leu  
165 170 175

Glu Tyr Val Ser Val Asp Gly Gly Ile Val Leu Ser Ile Glu Ser Met  
180 185 190

Lys Arg Leu Asn Ser Leu Leu Ser Val Pro Glu Lys Cys Pro Glu Gln  
195 200 205

Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala Val Cys  
210 215 220

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Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala Asp Gly  
225 230 235 240

Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Phe Ile Lys Glu Ala  
245 250 255

Met Thr Asn Gln Pro Asn Gln Val Val Glu Gly Cys Cys Ser Asp Met  
260 265 270

Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln Met His Val Met Met  
275 280 285

Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly His Val Phe Asn Asp Ala  
290 295 300

Leu Val Phe Leu Pro Pro Asn Gly Ser Glu Asn Asp  
305 310 315

<210> 4

<211> 1432

<212> DNA

<213> Mus musculus

<400> 4

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gtgatgcttg gaagcatctt ctgtgccttg atcactatgc taggccacat taggattgga	180
aacagaatgc accaccatga gcatcaccat ctgcaagccc ctaacaaaga cgatatctcg	240
aaaatttcag aggctgaacg catggagctc agtaagagtt tccgggtata ctgtatagtt	300
cttgtaaaac ccaaagatgt gagtctttgg gctgcagtga aggagacttg gaccaaacac	360
tgtgacaaag cagaattctt cagttctgaa aatgtttaaag tgtttgagtc aattaatatg	420
gacacaaatg acatgtgggt gatgatgagg aaagcttaca aatatgctta tgatcaatac	480
agggaccaat acaactgggt cttccttgca cgccccacta ctttcgctgt tattgaaaac	540
ctcaaatatt ttttgtaaa aaaggatcaa tcccaacctt tctatctcgg acacactgta	600
aaatctggag accttgaata tgtgagtgtg gatggaggaa ttgtcttaag catagaatca	660
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ttcattaaag aggcaatgac taaccaacca aaccaggtag tagaaggctg ttgctctgat    900
atggctgtta ctttcaatgg actgactcct aatcagatgc acgtgatgat gtatggggtg    960
taccggctta gggcatttgg acatgttttc aatgatgcat tggttttcctt acctccaaat   1020
ggttctgaga atgactgaca gaaagcaaga gcatgcattt agtaactata ttacgacatg   1080
gtatcatttt taattgatga cagatctaac atagtaatat gattctttttt cttatctttt   1140
accattgaa gtctgcttgt acaatgtcaa atggaatgct gtttttcctt tatatcattc   1200
ctgagaaatt aaaatgtatt aaaaataaat gttttaaaaa tagcaattttt tcaaacacat   1260
atttataagt atatttatgt gataaagact aaattataga cattgtaatc tgtgggtgat   1320
ctttgcttat tggtttttaa cttatgtatc attttagctt tgtaatatat gtaaatagaga   1380
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<210> 5

<211> 313

<212> PRT

<213> Brachydanio rerio

<400> 5

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Ile Phe Cys Leu Ile Met Ser Phe Phe Glu Thr Phe Asn Pro Gly Thr
          20          25          30

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His Ser Glu Gly His Asn His Leu His His His Leu Lys Pro Val Ser
          35          40          45

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Lys Asp Glu Leu Gln Lys Leu Ser Glu Ser Gln Met Ser Glu Phe Ala
          50          55          60

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Met Gln Val Arg Val Tyr Cys Leu Ile Met Val Thr Pro Lys Leu Leu
          65          70          75          80

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Val His Trp Ala Thr Ala Asn Asp Thr Trp Ser Lys His Cys Asp Lys

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90 95

85

Ser Val Phe Tyr Thr Ser Glu Ala Ser Lys Ala Leu Asp Ala Val Asp  
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Leu Gln Glu Gln Asp Glu Trp Thr Arg Leu Arg Lys Ala Ile Gln His  
115 120 125

Ala Tyr Glu Asn Ala Gly Asp Leu His Trp Phe Phe Ile Ala Arg Pro  
130 135 140

Thr Thr Phe Ala Ile Ile Glu Asn Leu Lys Tyr Leu Val Leu Asp Lys  
145 150 155 160

Asp Pro Ser Gln Pro Phe Tyr Ile Gly His Thr Glu Lys Ser Gly Glu  
165 170 175

Leu Asp Tyr Val Glu Tyr Asp Ser Gly Ile Val Leu Ser Tyr Glu Ala  
180 185 190

Met Arg Arg Leu Met Glu Val Phe Lys Asp Glu Asp Lys Cys Pro Glu  
195 200 205

Arg Gly Arg Ala Leu Trp Lys Met Ser Glu Glu Lys Gln Leu Ala Thr  
210 215 220

Cys Leu Lys Tyr Ser Gly Val Phe Ala Glu Asn Gly Glu Asp Ala Gln  
225 230 235 240

Gly Lys Gly Leu Phe Asn Lys Lys Ser Val Ser Ser Leu Ile Ser Asp  
245 250 255

Ser Ile Ser Gln Asn Pro Gly Asp Val Val Glu Ala Cys Cys Ser Asp  
260 265 270

Met Ala Ile Thr Phe Ala Gly Met Ser Pro Ser Gln Ile Gln Val Leu  
275 280 285

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290 295 300

Ser Leu Thr Phe Leu Pro Pro Arg Leu  
305 310

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<210> 6

<211> 1223

<212> DNA

<213> Brachydanio rerio

<400> 6

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acctttaatc caggaacca ctcagaaggt cacaatcacc tccaccatca tttgaaacct	180
gtcagcaaag atgagctaca gaagttatcc gagtctcaga tgtctgagtt cgctatgcag	240
gttcgagttct actgcctcat catggtcact ccaaagcttt tagttcactg ggcgacagct	300
aacgacacct ggagcaaaca ctgcgacaaa tctgtgtttt acacctctga ggcgctctaaa	360
gctctagatg cggttgacct acaggagcag gacgagtggg caaggcttcg caaagccatc	420
caacacgctt atgagaacgc cggagacctg cactggtttt tcatagcgcg acccaccacc	480
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tacattggcc acacggaaaa gtctggagag ctggattatg tggagtacga cagtgggatt	600
gtgttgagtt atgaagcgat gaggaggctg atggagggtg ttaaagatga agataaatgt	660
ccagagcgag gacgagctct atggaagatg tctgaagaaa agcaactggc cacttgtctg	720
aagtacagcg gagtggtttgc tgaaaacgga gaggacgccc aaggcaaagg gctttttaac	780
aagaagagtg tgagctcttt gatttccgat agcatcagcc aaaaccggg cgatgtggtg	840
gaggcctgtt gttctgacat ggctatcaca tttgctggga tgcgccgag tcagatacag	900
gtcttgatgt acggcgctcta cagacttcga ccgtacggac acgactttca cgattccttg	960
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aaaaaaaaa aaaaaaaaaa aaa	1223

<210> 7

<211> 316

<212> PRT



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<213> Rattus norvegicus

<400> 7

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Arg	Met	His	His	His	Glu	His	His	His	Leu	Gln	Ala	Pro	Asn	Lys	Asp	35	40	45	
Asp	Ile	Leu	Lys	Ile	Ser	Glu	Thr	Glu	Arg	Met	Glu	Leu	Ser	Lys	Ser	50	55	60	
Phe	Gln	Val	Tyr	Cys	Ile	Val	Leu	Val	Lys	Pro	Lys	Asp	Val	Ser	Leu	65	70	75	80
Trp	Ala	Ala	Val	Lys	Glu	Thr	Trp	Thr	Lys	His	Cys	Asp	Lys	Ala	Glu	85	90	95	
Phe	Phe	Ser	Ser	Glu	Asn	Val	Lys	Val	Phe	Glu	Ser	Ile	Asn	Met	Asp	100	105	110	
Thr	Asn	Asp	Met	Trp	Leu	Met	Met	Arg	Lys	Ala	Tyr	Lys	Tyr	Ala	Tyr	115	120	125	
Asp	Lys	Tyr	Lys	Asp	Gln	Tyr	Asn	Trp	Phe	Phe	Leu	Ala	Arg	Pro	Thr	130	135	140	
Thr	Phe	Ala	Val	Ile	Glu	Asn	Leu	Lys	Tyr	Phe	Leu	Leu	Arg	Lys	Asp	145	150	155	160
Pro	Ser	Gln	Pro	Phe	Tyr	Leu	Gly	His	Thr	Val	Lys	Ser	Gly	Asp	Leu	165	170	175	
Glu	Tyr	Val	Ser	Val	Asp	Gly	Gly	Ile	Val	Leu	Ser	Ile	Glu	Ser	Met	180	185	190	
Lys	Arg	Leu	Asn	Gly	Leu	Leu	Ser	Val	Pro	Glu	Lys	Cys	Pro	Glu	Gln	195	200	205	

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Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala Val Cys  
 210 215 220

Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala Asp Gly  
 225 230 235 240

Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Phe Ile Lys Glu Ala  
 245 250 255

Met Thr Asn Gln Pro Asn Gln Val Val Glu Gly Cys Cys Ser Asp Met  
 260 265 270

Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln Met His Val Met Met  
 275 280 285

Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly His Val Phe Asn Asp Ala  
 290 295 300

Leu Val Phe Leu Pro Pro Asn Gly Ser Glu Asn Asp  
 305 310 315

<210> 8

<211> 1283

<212> DNA

<213> Rattus norvegicus

<400> 8

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acttggaacca aacactgtga caaagcagaa ttcttcagtt ctgaaaatgt taaagtgttt	240
gagtcaatta atatggacac aaatgatatg tggttgatga tgaggaaagc ttacaaatat	300
gcttatgata aatacaagga ccaatacaac tggttcttcc ttgcacgccc cactactttc	360
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gaacaaggag gaatgatttg gaagatatct gaagataagc agctagcagt ctgcctgaaa	600

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aaatctgttg ggctTTTcat taaagaggca atgactaacc aaccaaacca ggtagtagaa	720
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ttcttacctc cgaatggTtc tgagaatgac tgacagaaag caagagcatg cTTttagtaa	900
ctatattaag acacggTatt gTTTTaatt gataacaaat ctaacacagt agtatgtTtc	960
TTTTtcttat ctggTtacac tggTataatc acacattgaa gtctactTgt acattgtcaa	1020
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ctaaattata gacattaaaa tctgtggTgt atctttgctt attggTTTta tacctgtgta	1200
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TTTggtcctt acctccgagg gaa	1283

<210> 9

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Completely synthesized.

<400> 9

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<210> 10

<211> 20

<212> DNA

<213> Artificial sequence

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<223> Completely synthesized.

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<210> 11

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<212> DNA

<213> Artificial sequence

<220>

<223> Completely synthesized.

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<210> 12

<211> 69

<212> DNA

<213> Artificial sequence

<220>

<223> Completely synthesized.

<400> 12

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tcacttttg

69

<210> 13

<211> 12

<212> PRT

<213> Artificial sequence

<220>

<223> Completely synthesized.

<400> 13

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5

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<210> 14

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Completely synthesized.

<400> 14

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<210> 15

<211> 18

<212> PRT

<213> Artificial sequence

<220>

<223> Completely synthesized.

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Ile Phe

<210> 16

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Completely synthesized.

<400> 16

7148.003 Sequence Listing.ST25

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